**REMARKS**

The Office Action has been carefully reviewed. No claim is allowed. Claims 7, 8, 20 and 22-45 presently appear in this application, with claims 20 and 22-31 being withdrawn from consideration, and define patentable subject matter warranting their allowance. Reconsideration and allowance are hereby respectfully solicited.

Claims 7, 8 and 32-34 have been rejected under 35 U.S.C. §112, first paragraph, as failing to comply with the written description requirement (new matter). This rejection is obviated by the amendment to claim 7 to replace the recitation of "4-55" amino acid residues with "5-9" amino acid residues.

The amendment to claim 7 is supported in the present specification at:

> Paragraph [0031]: "(a) a sequence which is a continuous stretch of at least 5 amino acids present in native EDG3 in positions of 135 to 154"; and
>
> Paragraph [0045]: "In accordance with the angiogenesis aspect of the invention this term refers to short sequences present in positions 135-154 of EDG3 receptor".

Reconsideration and withdrawal of the rejection are therefore respectfully requested.

Claims 7, 8 and 32-34 have been rejected under 35 U.S.C. §112, second paragraph, as being indefinite. This rejection is obviated by the amendment to claim 7.

Reconsideration and withdrawal of the rejection are therefore respectfully requested.

The amendments to claims 33 and 34 are merely being made to specifically identify the compounds (peptides) depicted in Fig. 1 (Figs. 1A and 1B), as originally claimed, by their SEQ ID NOs.

New claims 35-45 are added and the recitation of "5-9 amino acid residues" is supported in the specification as follows:

> Paragraph [0045]: "For example, if in a specific TM receptor such as EDG3, the positions corresponding to amino acid residues 142-150 in rhodopsin are 143-151 in the peptide, the continuous stretch of at least 5 amino acids may be from amino acid at position 143 to 147, from 144 to 148, from 145 to 149, etc. The continuous sequence may be of 5, 6, (for example 143-148, ….146 to 151), 7 (143-149 …, 145-151), 8, 9 amino acids. Preferably the sequences are of 6 amino acids.";
>
> Paragraph [0067]: "(b) determining the unique region of the 7TM receptor by aligning the sequence of the 2nd intracellular loop of rhodopsin of the 7TM receptor determined in (i) with the sequence, and determining the sequence of the specific 7TM receptor corresponding to positions 142-150 of rhodopsin ("unique region");
>
> (c) determining a continuous stretch of at least 5 amino acids of any of the unique regions above that is shorter than the length of the full unique region and modulates the 7TM receptor-associated signal transduction, by synthesizing a plurality of subsequences (optionally partially overlapping subsequences) of 5-9 aa obtained from the

> unique region; testing those subsequences in a test assay for determining signal transduction associated with the 7TM receptor, and selecting those subsequences that modulated said signal transduction associated with the 7TM receptor;"; and
>
> Paragraph [0070]: "Finding these short subsequences is a routine procedure, which can be achieved by several possible manners, such as by synthesizing subsequences of 5-9 aa having partially overlapping, or adjacent sequences, and optionally optimizing the chosen sequence (if rather longer sequences such as, for example, 8-9 aa are used) by sequentially deleting from one or both of its terminal amino acids until the optimal shorter sequence. The sequence chosen is not necessarily the shortest, but the best wherein a combination of best activity and shortest sequences are both taken into consideration."

No new matter is introduced by these amendments to the claims.

In view of the above, the claims comply with 35 U.S.C. §112 and define patentable subject matter warranting their allowance. Favorable consideration and early allowance are earnestly urged.

Respectfully submitted,

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